36. (New) The isolated polypeptide of claim 33 wherein said polypeptide comprises a sequence selected from the group consisting of SEQ ID NO: 2, 4 and 6.

37. (New) An isolated polypeptide comprising a polypeptide whose amino acid sequence is selected from the group consisting of SEQ ID NO: 2, 4 and 6.

REMARKS

Claims 1-24 are pending in the case. Claims 1-8 have been rejected.

Restriction/Election

Claims 1-24 are subject to a restriction requirement. Applicant has previously elected the claims of Group 1 (claims 1-8) and this requirement has now been made final. Applicant reaffirms the election of the claims of Group 1. Claims 1-8 have been cancelled without prejudice and new claims 25 – 37 have been added, which newly added claims track the claims of Group 1.

Informalities

The disclosure was objected to because of the inadvertent inclusion of a hyperlink (URL) in the specification. Applicant has amended the specification to delete this reference and has submitted a new paragraph without it. The amendment to the paragraph is shown in the edited version of the paragraph attached as an appendix hereto.

Rejection Under 35 U.S.C. §112

Claims 1-8 stand rejected under section 112 (second paragraph) as being indefinite because of use of a recitation of an amino acid sequence at least 75% identical to sequences contained in the sequence listing.

In response, Applicants have cancelled claims 1-8 without prejudice and have added new claims 25-37. New claim 25 is directed to an isolated polypeptide comprising a polypeptide with at least a 75% identity to SEQ ID NO: 4 and wherein the sequence identity differs only by conservative amino acid substitutions. (See application at page 23, lines 15-17). New claims 26 and 27 depend from claim 25. Thus, these claims are fully supported in the application as filed. In addition, the meaning of conservative amino acid substitutions is known in the art (see the Bentle Patent cited in the Office Action regarding obviousness).

Claims 5 through 8 have been rejected under section 112 because they depend from rejected claim 1. New claim 28 includes the limitations of claims 1 and 5-7. Thus, this claim is fully supported in the application. New claims 29 and 30 depend from claim 28 so that new claims 28 – 30 are believed to avoid the rejection under section 112. In addition, new claims 31-32 are similar to claim 28 but limited to Group B streptococci and, specifically, *S. agalactiae*.

New claim 37 is directed to polypeptides comprising the actual sequences of SEQ ID NO: 2, 4 and 6.

In view of these amendments, these claims are believed to be more definite and to fulfill the requirements of section 112, second paragraph, by better describing the claimed invention.

The Office Action also notes that the claims fail to state whether the sequences need be contiguous within the recited reference sequences. Applicant responds that

sequence identity is defined in the application at page 10, starting at line 12, and does not require the residues be contiguous (i.e., it allows for gaps in the compared sequences).

Further, new claims 28 and 31 are directed to isolated polypeptides otherwise found in the indicated microorganisms and thus the claims now recites "present in" rather than "found in" used in cancelled claim 5.

In view of these amendments, Applicants believe that this ground of rejection has been overcome and should be withdrawn.

Rejection Under 35 U.S.C. §102

Claims 1-3, 5 and 7 have been rejected under section 102(a) based on the Spellerberg et al reference.

Applicant responds that the sequences disclosed in Spellerberg et al are contended in the Office Action to be homologous to SEQ ID NO: 2 and 6 whereas new claim 25 recites only SEQ ID NO: 4 while new claim 37 recites the actual sequences of SEQ ID 2, 4 and 6. In addition, the other new claims require additional limitations not found in Spellerberg et al.

In view of these amendments and the foregoing arguments, Applicants believe that this ground of rejection has been avoided.

Rejection Under 35 U.S.C. §103

Claims 1-5 and 7 have also been rejected based on obviousness as being unpatentable over Spellerberg et al in view of the Bentle patent (US/4,694,073). It is contended in the office action that, while the sequence of Spellerberg and SEQ ID NO: 6 are not exact, those skilled in the art would have been motivated to determine the equivalent activity of both proteins because of the similarity in structure and because of the teaching of the Bentle patent that substitutions in somatostatin of conservative amino acid changes would render the activities of the bacterial proteins similar.

In response, Applicants note that Spellerberg et al (1999) is directed to finding a protein that binds to human laminin and recites the fact that this protein is 822 amino acids long and was able to reduce adherence of the wild-type *S. agalactiae* protein to immobilized human laminin. However, new claim 25 no longer recites SEQ ID NO: 6 and new claim 28 no longer recites Group B streptococci. New claim 31 recites an isolated polypeptide present in Group B streptococci, at least 75% identical to SEQ ID NO: 6 where the differences arise from conservative amino acid substitutions and the polypeptide reacts with authentic anti-Sp36 antibodies (See Example 4 at page 29-30 of the application). Conversely, Spellerberg et al only teach that their protein reacts with human laminin and that it may be responsible for attachment of streptococcal organisms to damaged epithelium (see Abstract) but do not indicate that it is immunologically reactive with an authentic antiserum generated in an animal (the rabbit of Example 4) against Sp36 protein.

In addition, the references do not make this claim element obviousness absent some experimental data whereas a reference offered to show obviousness must render each element of the claim obviousness, either separately or in combination. Applicants also note that the reaction demonstrated by Spellerberg was the reaction of histidine-tagged recombinant protein with immobilized human laminin and not laminin actually present on cells in a human and there is no mention of immunological activity of the protein studied by Spellerberg et al.

The Commissioner is requested to charge any additional fees, or credit any refunds, to Deposit Acc't No. 03-0678.

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Respectfully submitted,

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AMENDED SPECIFICATION

The paragraph beginning at page 28, line 13, has been amended as follows:

Sequence comparisons of the Sp36 encoded protein sequence against the publicly available GenBank sequence database (including the unfinished microbial database ~~(http://www.ncbi.nlm.nih.gov/BLAST/unfinishedgenome.html)~~) revealed two highly homologous amino acid sequences. One of these was a predicted amino acid sequence from the *S. pyogenes* genome. This predicted polypeptide comprised 825 amino acid residues (MW = 92,616 Da) that was 25.1% identical to the Sp36 amino acid sequence from pneumococcus serotype 4 but maintained the 5 histidine triads (underlined in Figure 5(a) - SEQ ID NO: 2). The second polypeptide encoded within the *S. pyogenes* database contained several errors that were corrected by our sequencing of this region of the genome. The DNA fragment obtained encoded a protein of 792 amino acids (MW = 87,457 Da) that was 12.6% identical to the pneumococcal sequence and 12.5% identical to the first *S. pyogenes* polypeptide. This predicted amino acid sequence contained four histidine triad motifs (underlined in Fig. 5(b) – SEQ ID NO.: 4). The third polypeptide sequence obtained was one already in the database (Accession No. AF062533) and identified only as an unknown gene downstream from a gene identified as *lmb* in *S. galactiae*. This 822 amino acid protein thus has a predicted molecular weight of 92,353 Da and maintains the 5 histidine triad motifs (underlined in Figure 5(C) - SEQ ID NO: 6). This second polypeptide shows 25.6% sequence identity to Sp36 of pneumococcus type 4 and 97.7% and 11.6% identity to the two group A homologs, respectively.